

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Rao, Aragula Gururaj
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134D

<150> US 60/092,936
 <151> 1998-07-25

<150> US 60/135,391
 <151> 1999-05-21

<150> US 09/352,159
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 ggaggacgcc cgagaagcct tggtcgcgcc accacggctt gtcccatcac aagactatct 240
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu

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ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac				288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	85	90	95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag				336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	100	105	110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc				384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	115	120	125	
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Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	130	135	140	
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	145	150	155	160
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	165	170	175	
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	180	185	190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg				624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	195	200	205	
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Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	210	215	220	
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Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	245	250	255	
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Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu	260	265	270	
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Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	275	280	285	
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Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
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Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
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gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
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Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	85	90	95
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Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	115	120	125
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	130	135	140
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Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	165	170	175
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	180	185	190
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Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	325	330	335
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Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	435	440	445
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
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ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
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ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac      288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
             85             90             95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag      336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
             100             105             110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc      384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
             115             120             125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg      432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
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ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg      480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
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cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
             165             170             175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
             180             185             190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
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Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
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Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
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ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp		
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Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln
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<212> PRT

<213> *Exophiala spinifera*

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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
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Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
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Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
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Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
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Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
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Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	130				135						140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145					150					155				160	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
			165					170						175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
			180				185						190		
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
		195				200						205			
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Ala	Cys	Gly	Val	Val	Ser	Gly	Gly
	210				215						220				
Gly	Leu	Val	Ser	Gln	Trp	Ser	Phe	Gln	Val	Cys	Ser	Arg	Phe	Ala	Met
225					230					235				240	
Pro	Cys	Gln	Arg	Asn	Leu	Phe	Gln	Ala	Gln	Cys	Thr	Ser	Thr	Pro	Pro
			245						250					255	
Ser	Leu	Lys	Leu	Ser	Ser	Arg	His	Pro	Ala	Val	Gln	Tyr	Asp	Arg	Pro

	260		265		270										
Arg	Ala	Pro	Cys	Ser	Glu	Ala	Lys	Arg	Trp	Trp	Phe	Arg	Tyr	Arg	Gln
	275						280						285		
Pro	Cys	Ile	Pro	Pro	His	Phe	His	His	Leu	Phe	Pro	Pro	Arg	Ser	Lys
	290						295						300		
His	Trp	Arg	Lys	Ile	Leu	Ser	Trp	Ala	Thr	Ile	Ala	Arg	Ser	Ser	Tyr
305					310						315				320
Gly	Thr	Ser	Arg	Gly	Gly	Ala	Asn	Lys	Ala	Ser	Arg	Ala	Ser	Ser	Asn
				325						330					335
Arg	Ala	Val	Thr	Pro	Ser	His	Leu	Pro	Glu	Ile	Pro	Ala	Ser	Thr	Ser
				340						345					350
Ile	Asp	Asn	Gly	Pro	Leu	Pro	Val	Ser	Trp	Ser	Glu	Thr	Arg	Asp	Gly
	355						360						365		
Ser	Gly	Pro	Asn	Ser	Pro	Ser	Arg	Tyr	Asp	Lys	Ser	Leu	Ser	Gly	Thr
	370						375						380		
Asn	Ser	Ala	Gln	Pro	Thr	Arg	Thr	Pro	Gly	Pro	Lys	Ser	Gln	Ser	Arg
385					390						395				400
Pro	Thr	Cys	Ser	Lys	Ser	Ser	Gly	Arg	Ser	Ser	Ser	Ile	Ser	Lys	Glu
				405						410					415
Leu	Arg	Ala	Pro	Ser	Met	Gly	Thr	Ile	Ser	Ser	His	Trp	Val	Arg	Arg
				420						425					430
Ser	Glu	Arg	Arg	Ser	Arg	Val	Phe	Ile	Ser	Leu	Glu	Arg	Arg	Arg	Leu
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Phe	Gly	Lys	Gly	Ile	Trp	Lys	Gly	Pro	Tyr						
	450						455								

<210> 10
 <211> 1392
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1389)

 <221> misc_feature
 <222> (1)...(3)
 <223> Extra lysine in K:trAPAO

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	

65	70	75	80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac				480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc				528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc				576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc				624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc				672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc				720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg				768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc				816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa				864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc				912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	290	295	300	

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc 960
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac 1008
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga 1056
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg 1104
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 1200
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1389
 Gln Arg Gly Ala Ala Glu Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

tag 1392

<210> 11
 <211> 463
 <212> PRT
 <213> Exophiala spinifera

<400> 11
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
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 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu

65					70					75				80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100						105				110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165					170						175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
	195						200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245					250						255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330						335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405					410						415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12
 ggggaattca aagacaacgt tgcggacgtg gtag 34

 <210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

 <400> 13
 ggggcggccg cctatgctgc tggcaccagg ctag 34

 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide for 3' RACE, N21965

 <400> 14
 tggtttcgtt accgacaacc ttgtatccc 29

 <210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide for 5' race, N21968

 <400> 15
 gagttggtcc cagacagact tttgtcgt 28

 <210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

 <220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

 <221> CDS
 <222> (1)...(1662)

 <400> 16
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 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa	96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln	
-70 -65 -60	
att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc	144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg	192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta	240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg	288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc	336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat	384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg	432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc	480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag	528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	

155	160	165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180			816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 185 190 195			864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 200 205 210 215			912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 220 225 230			960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln 235 240 245			1008
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg 250 255 260			1056
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu 265 270 275			1104
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn 280 285 290 295			1152
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro 300 305 310			1200
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp 315 320 325			1248
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp 330 335 340			1296
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln 345 350 355			1344
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala 360 365 370 375			1392
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu 380 385 390			1440

gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
410 415 420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp	
425 430 435	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca	1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala	
440 445 450 455	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c	1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala	
460 465	

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)

<400> 17																
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Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
		-70					-65						-60			
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
	-55					-50					-45					
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	-40				-35					-30						
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
	-25			-20					-15					-10		
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala	
		-5							1				5			
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	
	10						15					20				
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	
	25					30					35					
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	
	40			45					50					55		
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	
		60						65						70		
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	
		75					80					85				
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	
	90					95						100				
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	
	105					110					115					
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	

120		125		130		135									
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val
		140			145								150		
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu
		155						160					165		
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His
		170						175					180		
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly
		185					190				195				
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg
200				205						210				215	
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu
			220						225					230	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln
		235						240					245		
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg
		250					255					260			
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
		265					270				275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280				285						290				295	
Ser	Ile	Leu	Gly	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	
			300					305					310		
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
		315						320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
		330					335				340				
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
		345				350				355					
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360				365						370				375	
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
			380						385					390	
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
		395						400					405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
		410					415					420			
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
		425				430					435				
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
440				445						450				455	
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
			460					465							

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<221> CDS

<222> (1)...(2076)

<221> misc_feature
 <222> (1)...(687)
 <223> gst fusion + polylinker

<221> misc_feature
 <222> (688)...(2076)
 <223> K:trAPAO

<221> misc_feature
 <222> (688)...(690)
 <223> Extra lysine

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 1 5 10 15
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc	720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt	768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act	816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
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Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	

405										410										415										
ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggg	ctc	agt	aat	att	ttc	tcg		1296													
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser															
			420						425				430																	
gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tcg	aaa	aca	ggg	atg	cag		1344													
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln															
		435					440					445																		
tcg	att	tcg	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac		1392													
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His															
	450					455					460																			
ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca		1440													
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr															
	465				470				475						480															
gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt		1488													
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val															
			485					490					495																	
tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt		1536													
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu															
		500					505					510																		
ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat		1584													
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr															
	515					520					525																			
agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc		1632													
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly															
	530					535					540																			
ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga		1680													
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg															
	545				550				555					560																
gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg		1728													
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met															
			565					570					575																	
gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga		1776													
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg															
			580				585						590																	
caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg		1824													
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly															
	595					600					605																			
gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag		1872													
Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys															
	610					615			620																					
cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat		1920													
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp															
	625				630				635					640																

ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
660 665 670	
gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu	
675 680 685	
gtg cca gca gca tag	2079
Val Pro Ala Ala	
690	

<210> 19
 <211> 692
 <212> PRT
 <213> Unknown

<400> 19

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20 25 30	
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	


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<220>
<223> Nucleotide sequence of K:trAPAO translational
      fusion with barley alpha amylase signal sequence,
      for expression and secretion of the mature trAPAO
      in maize. Nucleotides 1-72, barley alpha amylase
      signal sequence, nucleotides 73-75, added lysine
      residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

<221> CDS
<222> (1)...(1461)

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
               -20                      -15                      -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
               -5                      1                      5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
               10                      15                      20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
               25                      30                      35                      40

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac      240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
               45                      50                      55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc      288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
               60                      65                      70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act      336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
               75                      80                      85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
               90                      95                      100

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tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 105 110 115 120	432
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 125 130 135	480
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 140 145 150	528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 155 160 165	576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 170 175 180	624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 185 190 195 200	672
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 205 210 215	720
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 220 225 230	768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser 235 240 245	816
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 250 255 260	864
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 265 270 275 280	912
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 285 290 295	960
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 300 305 310	1008
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 315 320 325	1056
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 330 335 340 345 350	1104

330	335	340	
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Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
345	350	355	360
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag			1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
	365	370	375
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag			1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
	380	385	390
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg			1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
	395	400	405
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag			1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
	410	415	420
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat			1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
	425	430	435
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg			1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
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 <211> 487
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

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 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
 10 15 20
 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
 25 30 35 40
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
 45 50 55
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
 60 65 70

Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr		
		75					80					85					
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro		
	90					95					100						
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu		
105					110					115					120		
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp		
				125					130					135			
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala		
				140				145					150				
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala		
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Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser		
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185					190					195					200		
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr		
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Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly		
			220					225					230				
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser		
			235				240					245					
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys		
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Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser		
265					270					275					280		
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu		
				285				290						295			
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg		
			300				305						310				
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser		
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Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr		
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Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys		
345					350					355					360		
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu		
				365				370						375			
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu		
			380				385					390					
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly		
		395					400					405					
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys		
	410					415					420						
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr		
425					430					435					440		
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val		
				445				450					455				
Ala	Ser	Leu	Val	Pro	Ala	Ala											
			460														

<210> 22
 <211> 1803
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS

<222> (1)...(1800)

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<400> 22
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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
  1           5           10           15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
          20           25           30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct      144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
          35           40           45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc      192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
          50           55           60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac      240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
          65           70           75           80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg      288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
          85           90           95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg      336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
          100          105          110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc      384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
          115          120          125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg      432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
          130          135          140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc      480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
          145          150          155          160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta      528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
          165          170          175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
          180          185          190

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta      624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
          195          200          205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
          210          215          220

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act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
225 230 235 240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg	768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245 250 255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa	816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
260 265 270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc	864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
275 280 285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta	912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
290 295 300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc	960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305 310 315 320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt	1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
325 330 335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
340 345 350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca	1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
355 360 365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
370 375 380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt	1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Thr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392

Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
450						455					460						
tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	1440	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
465					470					475					480		
acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	1488	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
				485					490					495			
aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	1536	
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr		
		500						505					510				
gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	1584	
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
		515					520					525					
gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	1632	
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
	530					535					540						
ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	ccg	ttc	1680	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
545					550					555					560		
aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	1728	
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
				565					570					575			
tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	caa	cga	ggg	gct	gca	gaa	gtt	1776	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		
			580					585					590				
gtg	gct	agc	ctg	gtg	cca	gca	gca	tag								1803	
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala										
		595				600											

<210> 23
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 23

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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val		
			20					25					30				
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro		
		35				40						45					
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys		
	50					55					60						
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr		
65					70					75					80		
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly		
				85					90					95			

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590
Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 24
<211> 3003
<212> DNA
<213> Unknown

<220>
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esp1 mat: an artificial spacer sequence and
K:trAPAO

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1575)
<223> esp1 mat

<221> misc_feature
<222> (1576)...(1611)
<223> spacer sequence

<221> misc_feature
<222> (1612)...(3000)
<223> K:trAPAO

<221> CDS
<222> (1)...(3000)

<221> misc_feature
<222> (1612)...(1614)
<223> Extra lysine

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-20 -15 -10
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
-5 1 5
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
10 15 20
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25 30 35 40

gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act	240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr	
45 50 55	
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu	
60 65 70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag ccg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	

265	270	275	280	
tac acg ttg gac aac gta acg gct gtg	tac cgt tct gaa acg gct cgc			960
Tyr Thr Leu Asp Asn Val Thr Ala Val	Tyr Arg Ser Glu Thr Ala Arg			
285	290	295		
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc				1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala				
300	305	310		
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat				1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr				
315	320	325		
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt				1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu				
330	335	340		
gga gca tat ccc att gga tcc cca ggg atc gga tgc cct caa gat cag				1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln				
345	350	355	360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc				1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile				
365	370	375		
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac				1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr				
380	385	390		
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg				1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val				
395	400	405		
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca				1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala				
410	415	420		
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc				1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala				
425	430	435	440	
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa				1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln				
445	450	455		
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt				1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val				
460	465	470		
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt				1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg				
475	480	485		
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc				1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly				
490	495	500		

agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val 505 510 515 520	1632
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	2304

730	735	740	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760			2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775			2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790			2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805			2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 810 815 820			2544
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 825 830 835 840			2592
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 855			2640
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 860 865 870			2688
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 875 880 885			2736
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 890 895 900			2784
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 905 910 915 920			2832
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 935			2880
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 940 945 950			2928
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 955 960 965			2976

gtg gct agc ctg gtg cca gca gca tag
 Val Ala Ser Leu Val Pro Ala Ala
 970 975

3003

<210> 25
 <211> 1000
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1) ... (24)

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 -5 1 5
 Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 60 65 70
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
 75 80 85
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
 90 95 100
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
 105 110 115 120
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 125 130 135
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 140 145 150
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 155 160 165
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 170 175 180
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
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 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
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 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
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 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 235 240 245
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
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 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 265 270 275 280
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
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 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
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Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile
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Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr
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Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val
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Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala
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Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala
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Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln
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Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val
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Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg
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Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
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Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
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Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
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Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
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Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
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Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
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Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
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Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
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Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
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Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 780 785 790
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
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 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 810 815 820
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
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 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 845 850 855
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 860 865 870
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
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 mature: artificial spacer: and K:trAPAO. For
 plant expression.

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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	
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Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
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Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
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ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
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Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
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Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	
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Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
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Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	
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Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	
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Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	
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Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	
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Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
235 240 245	
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac	864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
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Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	
265 270 275 280	
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Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	
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Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	
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Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	
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Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp	
330 335 340	
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Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	
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Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
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ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
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Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	

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Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
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Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
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Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
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Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
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Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
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Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
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Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu		
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ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	2160	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile		
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aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	2208	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
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Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala		
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Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
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gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	2352	
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Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
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caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	2592	
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
825					830					835					840		
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	2640	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
				845					850					855			
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Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
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gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	2736	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
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Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
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gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	2832
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925 930 935	

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940 945 950	

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	2973
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Gly Thr Ser Gly Asn Tyr Gly Leu Asp Ile Leu Ala Ala Leu Arg	
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Pro Gly Leu Thr Arg Pro	Leu Ala Thr Leu Ala Asp	Ser Ala Ala Ser
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Gly Glu Arg Leu Asp Ala	Asp Leu Ser Arg Leu Arg	Ser Thr Asp Pro
235	240	245
Ala Thr Leu Met Ala Arg	Ala Asp Ala Ala Arg	Pro Ala Ser Arg Asp
250	255	260
Leu Arg Arg Pro Arg Pro	Thr Gly Pro Ile Val	Asp Gly His Val Leu
265	270	275
Pro Gln Thr Asp Ser Ala	Ala Ile Ala Ala Gly	Gln Leu Ala Pro Val
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Arg Val Leu Ile Gly Thr	Asn Ala Asp Glu Gly	Arg Ala Phe Leu Gly
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Arg Ala Pro Met Glu Thr	Pro Ala Asp Tyr Gln	Ala Tyr Leu Glu Ala
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Gly Arg Ala Thr Pro Lys	Glu Met Val Ala Arg	Ile Phe Gly Asp Asn
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Gln Phe Asn Arg Gly Val	Ser Ala Phe Ser Glu	Ala Leu Val Arg Gln
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Gly Ala Pro Val Trp Arg	Tyr Gln Phe Asn Gly	Asn Thr Glu Gly Gly
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Arg Ala Pro Ala Thr His	Gly Ala Glu Ile Pro	Tyr Val Phe Gly Val
395	400	405
Phe Lys Leu Asp Glu Leu	Gly Leu Phe Asp Trp	Pro Pro Glu Gly Pro
410	415	420
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Gly Pro Gly Arg Thr Thr	Ile Asn Asp Leu Gly	Ala Ala Trp Ile Asn
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Glu Gly Glu Leu Gln Arg	Thr Thr Gly Asn Ser	Ile His Gln Ala Gln
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Asp Gly Thr Thr Thr Thr	Ala Pro Tyr Gly Asp	Ser Leu Leu Ser Glu
605	610	615
Glu Val Ala Ser Ala Leu	Ala Glu Leu Leu Pro	Val Trp Ser Gln Leu
620	625	630
Ile Glu Glu His Ser Leu	Gln Asp Leu Lys Ala	Ser Pro Gln Ala Lys

635	640	645
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn		
650	655	660
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu		
665	670	675
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile		
685	690	695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly		
700	705	710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala		
715	720	725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
730	735	740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
745	750	755
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr		
765	770	775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln		
780	785	790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
795	800	805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
810	815	820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
825	830	835
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
845	850	855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
860	865	870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
875	880	885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
890	895	900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
905	910	915
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu		
925	930	935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
940	945	950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
955	960	965

<210> 28

<211> 3618

<212> DNA

<213> Unknown

<220>

<223> gst:esp1:sp:K:trapao, 3618. 1-687, gst +
polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, 3616-3618, stop codon. For
bacterial expression.

<221> CDS

<222> (1)...(3615)

<221> misc_feature

<222> (1)...(687)
 <223> gst + polylinker

<221> mat_peptide
 <222> (688)...(2190)
 <223> esp1 mat

<221> misc_feature
 <222> (2191)...(2226)
 <223> spacer sequence

<221> misc_feature
 <222> (2227)...(3615)
 <223> K:trAPA0

<221> misc_feature
 <222> (2227)...(2229)
 <223> Extra lysine

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 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 atg ttg ggt ggt tgt cca aaagag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

145	150	155	160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta				528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac				576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc				624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt				672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg				720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	225	230	235	240
gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag				768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	245	250	255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct				816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	260	265	270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt				864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	275	280	285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att				912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	290	295	300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag				960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	305	310	315	320
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac				1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	325	330	335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg				1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	340	345	350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat				1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	355	360	365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct				1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	370	375	380	

gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp 385 390 395 400	1200
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggg gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg 435 440 445	1344
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460	1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510	1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515 520 525	1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545 550 555 560	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575	1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620 625 630 635 640	1872

610	615	620	
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640			1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655			1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670			2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675 680 685			2064
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700			2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720			2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly 725 730 735			2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val 740 745 750			2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765			2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780			2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800			2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815			2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830			2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845			2544

gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe 930 935 940	2832
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met 945 950 955 960	2880
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 965 970 975	2928
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990	2976
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 995 1000 1005	3024
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1010 1015 1020	3072
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1025 1030 1035 1040	3120
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055	3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070	3216
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 51	3264

1075	1080	1085	
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta			3312
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc			3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115 1120	
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg			3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac			3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt			3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa			3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
1170	1175	1180	
ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc			3600
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser			
1185	1190	1195 1200	
ctg gtg cca gca gca tag			3618
Leu Val Pro Ala Ala			
1205			

<210> 29
 <211> 1205
 <212> PRT
 <213> Unknown

<400> 29

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20 25 30			
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
35 40 45			
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
50 55 60			
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65 70 75 80			
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85 90 95			
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100 105 110			
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115 120 125			
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			

130		135		140
Gly Asp His Val Thr	His Pro Asp Phe Met	Leu Tyr Asp Ala Leu Asp		
145	150	155	160	
Val Val Leu Tyr Met	Asp Pro Met Cys Leu	Asp Ala Phe Pro Lys Leu		
	165	170	175	
Val Cys Phe Lys Lys	Arg Ile Glu Ala Ile	Pro Gln Ile Asp Lys Tyr		
	180	185	190	
Leu Lys Ser Ser Lys	Tyr Ile Ala Trp Pro	Leu Gln Gly Trp Gln Ala		
	195	200	205	
Thr Phe Gly Gly Gly	Asp His Pro Pro Lys	Ser Asp Leu Val Pro Arg		
	210	215	220	
Gly Ser Pro Glu Phe	Ala Pro Thr Val Lys	Ile Asp Ala Gly Met Val		
225	230	235	240	
Val Gly Thr Thr Thr	Thr Val Pro Gly Thr	Thr Ala Thr Val Ser Glu		
	245	250	255	
Phe Leu Gly Val Pro	Phe Ala Ala Ser Pro	Thr Arg Phe Ala Pro Pro		
	260	265	270	
Thr Arg Pro Val Pro	Trp Ser Thr Pro Leu	Gln Ala Thr Ala Tyr Gly		
	275	280	285	
Pro Ala Cys Pro Gln	Gln Phe Asn Tyr Pro	Glu Glu Leu Arg Glu Ile		
	290	295	300	
Thr Met Ala Trp Phe	Asn Thr Pro Pro Pro	Ser Ala Gly Glu Ser Glu		
305	310	315	320	
Asp Cys Leu Asn Leu	Asn Ile Tyr Val Pro	Gly Thr Glu Asn Thr Asn		
	325	330	335	
Lys Ala Val Met Val	Trp Ile Tyr Gly Gly	Ala Leu Glu Tyr Gly Trp		
	340	345	350	
Asn Ser Phe His Leu	Tyr Asp Gly Ala Ser	Phe Ala Ala Asn Gln Asp		
	355	360	365	
Val Ile Ala Val Thr	Ile Asn Tyr Arg Thr	Asn Ile Leu Gly Phe Pro		
	370	375	380	
Ala Ala Pro Gln Leu	Pro Ile Thr Gln Arg	Asn Leu Gly Phe Leu Asp		
385	390	395	400	
Gln Arg Phe Ala Leu	Asp Trp Val Gln Arg	Asn Ile Ala Ala Phe Gly		
	405	410	415	
Gly Asp Pro Arg Lys	Val Thr Ile Phe Gly	Gln Ser Ala Gly Gly Arg		
	420	425	430	
Ser Val Asp Val Leu	Leu Thr Ser Met Pro	His Asn Pro Pro Phe Arg		
	435	440	445	
Ala Ala Ile Met Glu	Ser Gly Val Ala Asn	Tyr Asn Phe Pro Lys Gly		
	450	455	460	
Asp Leu Ser Glu Pro	Trp Asn Thr Thr Val	Gln Ala Leu Asn Cys Thr		
465	470	475	480	
Thr Ser Ile Asp Ile	Leu Ser Cys Met Arg	Arg Val Asp Leu Ala Thr		
	485	490	495	
Leu Met Asn Thr Ile	Glu Gln Leu Gly Leu	Gly Phe Glu Tyr Thr Leu		
	500	505	510	
Asp Asn Val Thr Ala	Val Tyr Arg Ser Glu	Thr Ala Arg Thr Thr Gly		
	515	520	525	
Asp Ile Ala Arg Val	Pro Val Leu Val Gly	Thr Val Ala Asn Asp Gly		
	530	535	540	
Leu Leu Phe Val Leu	Gly Glu Asn Asp Thr	Gln Ala Tyr Leu Glu Glu		
545	550	555	560	
Ala Ile Pro Asn Gln	Pro Asp Leu Tyr Gln	Thr Leu Leu Gly Ala Tyr		
	565	570	575	
Pro Ile Gly Ser Pro	Gly Ile Gly Ser Pro	Gln Asp Gln Ile Ala Ala		
	580	585	590	
Ile Glu Thr Glu Val	Arg Phe Gln Cys Pro	Ser Ala Ile Val Ala Gln		

	1060		1065		1070
Arg	Asp Thr Ser Ile Asp Val	Asp Arg Gln Trp Ser	Ile Thr Cys Phe		
	1075	1080	1085		
Met	Val Gly Asp Pro Gly Arg Lys Trp Ser	Gln Gln Ser Lys Gln Val			
	1090	1095	1100		
Arg	Gln Lys Ser Val Trp Asp Gln Leu Arg	Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120		
Gly	Ala Gln Val Pro Glu Pro Ala Asn Val	Leu Glu Ile Glu Trp Ser			
	1125	1130	1135		
Lys	Gln Gln Tyr Phe Gln Gly Ala Pro Ser	Ala Val Tyr Gly Leu Asn			
	1140	1145	1150		
Asp	Leu Ile Thr Leu Gly Ser Ala Leu Arg	Thr Pro Phe Lys Ser Val			
	1155	1160	1165		
His	Phe Val Gly Thr Glu Thr Ser Leu Val	Trp Lys Gly Tyr Met Glu			
	1170	1175	1180		
Gly	Ala Ile Arg Ser Gly Gln Arg Gly Ala	Ala Glu Val Val Ala Ser			
1185	1190	1195	1200		
Leu	Val Pro Ala Ala				
	1205				

<210> 30

<211> 3591

<212> DNA

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1 or similar vector. gst:BEST1:sp:K:trAPAO fusion, 3591 nt.
1-687 gst
+ polylinker, 688-2163, BEST1 mature; 2164-2199, spacer, 2200-3588, K:trAPAO

<221> misc_feature

<222> (1)...(687)

<223> gst + polylinker

<221> mat_peptide

<222> (688)...(2163)

<223> BEST1 mature

<221> misc_feature

<222> (2164)...(2199)

<223> spacer sequence

<221> misc_feature

<222> (2200)...(3588)

<223> K:trAPAO

<221> CDS

<222> (1)...(3588)

<221> misc_feature

<222> (2200)...(2202)

<223> Extra lysine

<400> 30

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc	720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	

225	230	235	240	
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro	245	250	255	768
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	260	265	270	816
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	275	280	285	864
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	290	295	300	912
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys	305	310	315	960
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala	325	330	335	1008
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg	340	345	350	1056
cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly	355	360	365	1104
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser	370	375	380	1152
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln	385	390	395	1200
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe	405	410	415	1248
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro	420	425	430	1296
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu	435	440	445	1344
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg	450	455	460	1392

ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu 465 470 475 480	1440
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg 485 490 495	1488
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510	1536
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu 515 520 525	1584
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro 530 535 540	1632
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly 545 550 555 560	1680
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac ggc cgg gcc Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala 565 570 575	1728
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn 580 585 590	1776
cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605	1824
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gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625 630 635 640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645 650 655	1968
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala 660 665 670	2016
aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675 680 685	2064
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 685 690 695	2112

690	695	700	
gtg tgc ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala 705 710 715 720			2160
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn 725 730 735			2208
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr 740 745 750			2256
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala 755 760 765			2304
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly 770 775 780			2352
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn 785 790 795 800			2400
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu 805 810 815			2448
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 820 825 830			2496
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835 840 845			2544
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu 850 855 860			2592
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp 865 870 875 880			2640
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala 885 890 895			2688
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu 900 905 910			2736
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala 915 920 925			2784

acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat	2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr	
930 935 940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag	2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys	
945 950 955 960	
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att	2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile	
965 970 975	
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg	2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val	
980 985 990	
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc	3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro	
995 1000 1005	
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg	3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala	
1010 1015 1020	
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac	3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp	
1025 1030 1035 1040	
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc	3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser	
1045 1050 1055	
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga	3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg	
1060 1065 1070	
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg	3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp	
1075 1080 1085	
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc	3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu	
1090 1095 1100	
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac	3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn	
1105 1110 1115 1120	
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg	3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro	
1125 1130 1135	
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc	3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu	
1140 1145 1150	
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta	3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	

1155	1160	1165	
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Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly			
1170	1175	1180	
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 <211> 1196
 <212> PRT
 <213> Unknown

<400> 31

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		20					25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
	35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50				55						60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65				70					75						80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
			85					90						95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
		100					105						110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
	115					120						125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
			165					170						175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
		180					185						190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
	195					200						205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210				215						220				
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly
225					230					235					240
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro
			245					250						255	
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His
		260						265						270	
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp
	275						280					285			
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val
	290					295					300				
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys
305				310						315					320
Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Gly	Phe	Ala

785		790		795		800
Gln Ser Glu Val	Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly Glu				
	805	810			815	
Leu Gln Arg Thr	Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr					
	820	825		830		
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala						
	835	840		845		
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu						
	850	855		860		
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp						
865	870	875		880		
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala						
	885	890		895		
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu						
	900	905		910		
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala						
	915	920		925		
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr						
	930	935		940		
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys						
945	950	955		960		
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile						
	965	970		975		
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val						
	980	985		990		
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro						
	995	1000		1005		
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala						
	1010	1015		1020		
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp						
1025	1030	1035		1040		
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser						
	1045	1050		1055		
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg						
	1060	1065		1070		
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp						
	1075	1080		1085		
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu						
	1090	1095		1100		
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn						
1105	1110	1115		1120		
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro						
	1125	1130		1135		
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu						
	1140	1145		1150		
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu						
	1155	1160		1165		
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly						
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Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala						
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 <212> DNA
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<220>

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<222> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative
glycosylation sites

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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val	
195 200 205	

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
225 230 235 240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg	768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245 250 255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa	816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
260 265 270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc	864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
275 280 285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta	912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
290 295 300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc	960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305 310 315 320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt	1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
325 330 335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
340 345 350	
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
355 360 365	
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Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt	1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344

Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp		
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cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	1392	
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
	450					455					460						
tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	1440	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
465					470					475					480		
acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	1488	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
				485					490					495			
aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	1536	
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr		
			500					505					510				
gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	1584	
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
	515						520					525					
gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	1632	
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
	530					535					540						
ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	ccg	ttc	1680	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
545					550					555					560		
aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	1728	
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
				565					570					575			
tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	gaa	gtt	1776	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		
			580					585				590					
gtg	gct	agc	ctg	gtg	cca	gca	gca	tag								1803	
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	*									
		595					600										

<210> 33
 <211> 600
 <212> PRT
 <213> Unknown

<400> 33

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35				40						45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				

Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr	65	70	75	80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	85	90	95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	100	105	110	
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	115	120	125	
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	130	135	140	
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	145	150	155	160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	165	170	175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	180	185	190	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ala	Glu	Val	195	200	205	
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	210	215	220	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	225	230	235	240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	245	250	255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	260	265	270	
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	275	280	285	
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	290	295	300	
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	305	310	315	320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	325	330	335	
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	340	345	350	
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	355	360	365	
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	370	375	380	
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	385	390	395	400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	405	410	415	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	420	425	430	
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	435	440	445	
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	450	455	460	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	465	470	475	480
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	485	490	495	
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	500	505	510	
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	515	520	525	

68

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gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcacac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttggaacg	gagacgtctt	tagtttgga	agggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcca	1920
gcagcatag						1929

<210> 36

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 36

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
			115				120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	195					200						205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235					240
Pro	Tyr	Gly	Asp	Ser	Pro	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245						250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	Tyr	Ser	Leu	Glu
			260					265					270		
Asp	Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
	275					280						285			
Ala	His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Ser	Val
	290					295					300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305					310					315					320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser

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aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcattt	ggagggcgag	660
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agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gagggtgcaa	gtgcacttgc	840
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gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggacct	960
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taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	cagggtgcgtg	1140
cggtgtcctc	tcaggtaggg	gactcgtttc	ttagtgggtca	ttccaggtat	gcagtcgatt	1200
tgccatgcc	tgtcaaagga	acttgttcca	ggctcagtgc	acctcaacac	ccccgtcgct	1260
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tcgagctgtg	accccatctc	atttgccaga	gataccagca	tcgaagtcca	tcggcaatgg	1560
tccattacct	gtttcatggt	cggagaccgg	ggacggaagt	ggtcccaaca	gtccaagcag	1620
gtacgacaaa	agtcgtgtctg	ggaccaactc	cgcgcagcct	acgagaacgc	cggggcccaa	1680
gtcccagagc	cggccaacgt	gctcgaaatc	gagtgggtcca	agcagcagta	tttccaagga	1740
gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcacac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttggaacg	gagacgtctt	tagtttgga	agggatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctgggtgcca	1920
gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40						45		
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
		130				135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
		180					185						190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr

210		215		220
Thr Gly Asn Ser Ile	His Gln Ala Gln Asp Gly	Thr Thr Thr Thr Ala		
225	230	235	240	
Pro Tyr Gly Asp Ser	Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
	245	250	255	
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu				
	260	265	270	
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				
	275	280	285	
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val				
	290	295	300	
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile				
305	310	315	320	
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				
	325	330	335	
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				
	340	345	350	
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				
	355	360	365	
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala				
	370	375	380	
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				
385	390	395	400	
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				
	405	410	415	
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile				
	420	425	430	
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp				
	435	440	445	
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				
	450	455	460	
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile				
465	470	475	480	
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser				
	485	490	495	
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr				
	500	505	510	
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile				
	515	520	525	
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr				
	530	535	540	
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe				
545	550	555	560	
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly				
	565	570	575	
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val				
	580	585	590	
Val Ala Ser Leu Val Pro Ala Ala				
	595	600		

<210> 39
 <211> 1930
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
<222> (1134)...(1187)

<221> misc_feature
<222> (648)...(648)
<223> n = A,T,C or G

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gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgccaagc attcgccaat      180
ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac      240
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tttgcccttg acaggctccc tccttgcaag ctggtgccag tgcggcctt gtcttcacct      360
gaataacctt ttgaggttga tgccacggcg ctggtgccgg gacacacgac cccagacaac      420
gttgcggaag tggtagtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc      480
caggccgcgg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact      540
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc      600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag      660
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct      720
ccttatgggt actccttggt aagcacaaac ccactttgtg atgagacctc tgcgagtggt      780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc      840
ggaactcctc cccgtatggt ctcaagtgat cgaagagcat agccttcaag acctcaaggc      900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggaact      960
aaacttgctt gctgttctcg gcgtagcaaa ccagatcaca cgcgctctgc tcggtgtgga     1020
agcccacgag atcagcatgc tttttctcac cgaactacatc aagagtgcc aagggtctcag     1080
taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa cagggtgcgtg     1140
tggtgtcgtc tcagggtggg gactcgtttc tcaagtggtc atttcaggta tgcagtcgat     1200
ttgccatgcc atgtcaaagg aacttggttc aggcctcagt cacctcaaca cccccgtcgc     1260
tgaaattgag cagtcggcat ccggctgtac agtacgatcg gcctcgggcg ccgtgttccg     1320
aagcaaaaag gtggtggttt cgttaccgac aaccttgat cccacctga cattttcacc     1380
acctctcccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa     1440
gatagtcttc gtatgggaca agccgtgggt gcgcgaacaa ggcttctcgg gcgtcctcca     1500
atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg     1560
gtccattacc tgtttcatgg tcggagaccc gggacggaag tggteccaac agtccaagca     1620
ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca     1680
agtcccagag ccggccaacg tgctcgaaat cgagtggtcg aagcagcagt atttccaagg     1740
agctccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgctcagaac     1800
gccgttcaag agtgttcatt tcggttgaac ggagacgtct ttagtttgga aagggtatat     1860
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<210> 40
<211> 598
<212> PRT
<213> *Exophiala spinifera*

<220>
<221> VARIANT
<222> (216)...(216)
<223> Xaa = Any Amino Acid

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<400> 40
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20             25             30

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			500					505					510			
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	
		515					520					525				
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	
	530					535					540					
Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	
545				550						555					560	
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	
			565					570					575			
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	
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Ser	Leu	Val	Pro	Ala	Ala											
		595														

<210> 41
 <211> 1928
 <212> DNA
 <213> *Rhinocycladiella atrovirens*

<220>
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 <222> (739)...(811)

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 <222> (1134)...(1185)

<400> 41

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gacgcttcgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgccaagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattaccaa	gctcaattac	240
tacatcgctg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccg	tgccggccct	ggcttcacct	360
gaatacccct	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat	420
gttgcggacg	tggtcgtggt	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggctgccc	ggctgtcctg	cctcgcttct	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	gctatcaatg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
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taatattgtc	tcggataaga	aagacgggtg	gcagtatatg	cgatgcaaaa	cagggtgcgtg	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtgggtcat	tcaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
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cggtcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggatatatgg 1860
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cagcatag 1928

<210> 42
<211> 598
<212> PRT
<213> Rhinocycladiella atrovirens

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
180 185 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205
Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
225 230 235 240
Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
245 250 255
Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
260 265 270
Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
275 280 285
Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
290 295 300
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305 310 315 320
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
325 330 335
Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
340 345 350
Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
355 360 365
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
370 375 380

Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys	Val
385					390					395					400
Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro
				405					410					415	
Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly
			420					425					430		
Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu
		435					440					445			
Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe
	450					455				460					
Ala	Arg	Asp	Thr	Ser	Ile	Glu	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys
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Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln
				485					490					495	
Val	Arg	Gln	Lys	Ser	Val	Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn
			500					505					510		
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp
		515					520					525			
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Val	Val	Tyr	Gly	Leu
	530					535				540					
Asn	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly
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Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met
				565					570					575	
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala
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Ser	Leu	Val	Pro	Ala	Ala										
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<210> 43
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
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 <222> (739)...(811)

<221> intron
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ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300
tttgcccttg acaggctccc tccttgcaag ctgggtgccg tgccggccct ggcttcacct	360
gaatacctct ttgaggttga tgccacggcg ctgggtccag gacactcaac cccagacaat	420
gttgcggacg tggctcgtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc	480
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aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
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gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct	960

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gccatgccat gtcaaaggaa cttgtttccag gctcagtga cctcaacacc cccgtcgccg 1260
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cagcatag 1928

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<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
          35          40          45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
          50          55          60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
          65          70          75          80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
          85          90          95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
          100          105          110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
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Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
          130          135          140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
          145          150          155          160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
          165          170          175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
          180          185          190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
          195          200          205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
          210          215          220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
          225          230          235          240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
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Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
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Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
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 Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
 290 295 300
 Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
 305 310 315 320
 Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
 325 330 335
 Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
 340 345 350
 Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
 355 360 365
 Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
 370 375 380
 Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
 385 390 395 400
 Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 405 410 415
 Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 420 425 430
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 435 440 445
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
 450 455 460
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 465 470 475 480
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 485 490 495
 Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 500 505 510
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 515 520 525
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540
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<210> 45
 <211> 1928
 <212> DNA
 <213> *Rhinocycladiella atrovirens*

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cgttcaaggg	tggtcatttc	gttggaaacg	agacgtcttt	gggttggaag	gggtatatgg	1860
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cagcatag						1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocycladiella atrovirens

<400> 46

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Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
		35					40					45			
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
	50					55					60				
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
65					70					75				80	
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
				85					90					95	
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
				100				105					110		
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
		115					120					125			
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
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Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
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Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
				165					170					175	

Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
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Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe
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Lys	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
	210					215					220				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
225					230					235					240
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
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His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
	290				295						300				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
305					310					315					320
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
			325						330					335	
Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
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Gly	Met	Gln	Ser	Leu	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
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Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
	370					375					380				
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys
385					390					395					400
Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro	Leu
			405						410					415	
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Gly	Tyr	Tyr	Ser
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Lys	Ile	Val	Phe	Val	Asp	Lys	Leu	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser
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Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr
	450				455						460				
Ser	Ile	Glu	Val	Asp	Arg	Gln	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp
465				470						475					480
Pro	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val
			485					490						495	
Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro
		500						505					510		
Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe
	515					520						525			
Gln	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Cys	Leu	Asn	Thr	Leu	Gly
	530					535					540				
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly	Val	His	Phe	Val	Gly	Thr	Glu
545					550					555					560
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
			565					570						575	
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Pro	Ser	Leu	Val	Pro	Ala	Ala	
		580						585					590		

<210> 47
 <211> 600
 <212> PRT
 <213> Exophiala spinifera

<400> 47

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75					80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155					160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225				230						235					240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245						250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
		260					265						270		
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
	275						280					285			
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
	290					295					300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305				310						315					320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
			325						330					335	
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		340						345					350		
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
	355					360						365			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
	370					375					380				
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
385				390						395					400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
			405						410					415	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile
		420						425					430		
Leu	Gly	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	
	435					440					445				
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile

450		455		460
Ser Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480	
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser				
	485	490	495	
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr				
	500	505	510	
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile				
	515	520	525	
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr				
	530	535	540	
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe				
545	550	555	560	
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly				
	565	570	575	
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val				
	580	585	590	
Val Ala Ser Leu Val Pro Ala Ala				
	595	600		

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	

100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270			816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285			864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300			912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320			960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335			1008

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 49
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteine 461

<400> 49																	
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val		
			20				25						30				
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser		
		35					40					45					
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn		
	50				55					60							
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu		
65					70				75					80			
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
			85					90					95				
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu			
		100					105					110					
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Pro	Val	Trp	Ser	Gln	Leu			
		115					120										

Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	
305					310				315					320	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
450						455					460				

<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50

aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
1				5					10				15		

48

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggg ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 51
<211> 463

<212> PRT
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20					25					30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40					45			
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
	50				55						60				
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75					80
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
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Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
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	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
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Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
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Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
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Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
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Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385				390						395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly

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Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
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ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt	ctg	agc	tcc	ctc	gtt		96	
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Ser	Leu	Val			
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ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg		144	
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser			
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Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn			
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Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln			
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gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg		384	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu			
115			120						125									
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Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys			
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Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile		
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Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
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Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
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Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
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gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	912	
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
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caa	tcg	agc	tcc	gac	ccc	atc	tca	ttt	ggc	aga	gat	acc	agc	atc	gac	1008	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
				325					330					335			
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Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
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cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	1104	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
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gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	1152	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
	370					375					380						

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Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
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gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
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 <213> Unknown

<220>
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35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	

Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
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Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
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Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
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Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
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Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
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Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
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Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
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Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
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Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
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Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
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